

8#

TOBT2T" 2622E860

601-1-098CIP

I II
human EF2K 122 GEWLDEVLKMASQPFGRGAMRECFTKKLSNFLHAQ-----QWKGASNYVAKRYIEPVD
C. e. EF2K 108 KQWTEIDVDRLHPDSFARGAMRECYRLKKCSKHGTSQ-----DW--SSNYVAKRYICQVD
MHCK A 570 NKWIRLSMKLKVERKPPFAEGALREAYHTVSLGVGTDENYPLGTTTKLFPPIEMISPISKNNEAMTQLKNGTKFVLKLYKKEAE
MHCK B 130 AQWTCATLVKVEPVPFAEGAFAFRKAYHTLDLSKSGA-----SGRYVSKIGKK---
FC-AN09 1 IVCVSIEKTPFAKGSCTAHKLKDWSP-----DQGLVGKFFSTNKK-
consensus **W*****O*****F**G**R**O*****F*****O*****V**K*****

IV
human EF2K 178 ---RDVYFEDVRLQMEAKLWGEENRHRKPPKQVDIMQMCIIELKDR---PGKPLF-HLEHYIEGKYIKYNSNSGFVRDDNI
C. e. EF2K 162 ---RRVLFDDVRLQMDAKLWAEENRYNPPKKIDIVQMCVIE MIDV---KGSPLY-HLEHFIEGKYIKYNSNSGFVSNA--
MHCK A 653 QOASRELYFEDVKMQMVCRDWGNKFNQKKPPKKIEFLMSWVVELIDRSPSSNGQPILCSEPLLVGEFKKNSNYGAVLTN--
MHCK B 177 -PTPRPSYFEDVKMQMIAKKWADKYNSEFKPPKKIEFLQSCVLEFVDR TSSD---LICGAEPYVEGQYRKYNNSNGFVSND--
FC-AN09 42 --TTRDSYFTDVLMTFCAKWAEKFNKAKPPKPIITFLPSYVYELIDHPPPY---PV-CGGEPIEGDYKKNNSNGYVSSDA-
consensus ***R**OF*DV*OQ*****W*****ON***PPK*O*OO**OOEo*D*****O*****E*OO*G*O*K*N*N*G*V*****

VI
human EF2K 252 RLTPQAFSHFTFERSGHQLIVVDIQGVGDLYTDPQIHTETGTDFGDGDLGVGMALFFYSHACNRICESMGLAPDLSPRERD
C. e. EF2K 235 RLTPQAFSHFTFERSGHQMMVVDIQGVGDLYTDPQIHTVVGTDYGDGDLGVGMALFFHSHRNCNDICETMDLSNFE LSPPEIE
MHCK A 734 RSTPQAFSHFTYELSNKQMI VVDIQGVDDLYTDPQIHTPDGKGFGDLGNLGKAGINKFITT HKCNVAVCALLDL-DVKLG-----
MHCK B 254 RNTPQGSFHTYEHSHNQLLIIDIQGVGDHYTDPQIHTYDGVGFGI GNLGQKGFELDTHKCNVICQYI, NLQSN-----
FC-AN09 118 RNTPQGSFHSFYSYELSNHELLIVVDIQGVNDFYTDPQIHTKSGEGFEGE GNLGETGFHKFLQTHKCNPVCDFLKLPIN-----
consensus R*TPQ*FSHF*OE*S***OooooDIQGV*DoYTDPOIHT**G**OG*GNLG**Go**Fo**H*CN*OC**O*L**O*****

VII
human EF2K 335 AVNQNTKLLQSAKT--ILRGTEEEKCS
C. e. EF2K 318 ATEVAMEVAAKQKSCIVPPTVFEARR
MHCK A 811 ----GVLSGNNKKQ--LQQGTMVMPDI
MHCK B 330 -----PKSEKSDC---GTVPRPDL
FC-AN09 194 -----QSKKA--LLRGTLPPVVQL
consensus *****K*****T*****

Figure 1A

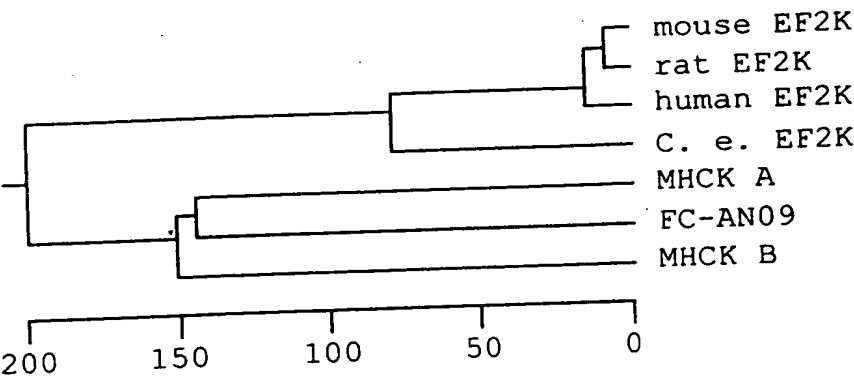
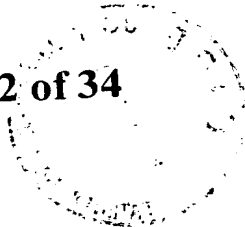


Figure 1B

601-1-098CIP

human eEF-2K	1R.....QSP.....DG....G.....E.....	44
C. elegans eEF-2K	1	MTIDTTNESDNTSPGLEASARTFSLNASKMVR-----ITD	38
mouse eEF-2K	1	MADEDLIFCLEGVDGGRCSRAGHNADSDTDSDDDEGYFICPITD	44
human eEF-2K	45	.PS.....N..NK.....S.RY.SS.....N.....Q....-	93
C. elegans eEF-2K	39	DYADEVFTEQNDVVIEKPRMD-----PLHVRKLMETWRKAARRART	79
mouse eEF-2K	45	DHMSNQNVSSKVQSYSNLTKECGS-TGSPASSEHFKEAWKHAIKAK-	92
human eEF-2K	94R.....D.....	143
C. elegans eEF-2K	80	NYIDPWDEFNIHEYPVQRAKRYSAIRKQWTEIDVVRILHPDSEFARGAM	129
mouse eEF-2K	93	HMPDPWAEFFHLEDIATEHATRHRYNAVTEGWLKDEVLIKMASQPFGRGAM	142
MHCK A	572	WIRLSMKLVKVERKPEFEGAL	591
human eEF-2K	144K.....	166
C. elegans eEF-2K	130	RECYRLKKCS-----KHGTSQDW--SSN	150
mouse eEF-2K	143	RECFRTKKLS-----NFLHAQQWKGASN	165
MHCK A	592	REAYHTVSLGVGTDENYPLGTTTKLFPPIEMISPISKNNNEAMTQLKNGTK	641
human eEF-2K	167D.....R.....E.....	212
C. elegans eEF-2K	151	YVAKRYICQVD-----RRVLFDDVRLQMDAKLWAEYNNRYNPPKKIDIVQM	196
mouse eEF-2K	166	YVAKRYIEPVD-----RSVYFEDVQLQMEAKLWGEDYNRRHKPPKQVDIMQM	211
MHCK A	642	EVLKLYKKEAEQQASRELYFEDVKMQMVCRDWGNKFNQKKPPKKIEFLMS	691
human eEF-2K	213K.....	256
C. elegans eEF-2K	197	CVIEMIDVK-----GSP-LYHLEHFIIEGKYIKYNSNSGVF-S-NAARLTPO	239
mouse eEF-2K	212	CIIEELKDRP-----GQP-LFHLEHYIEGKYIKYNSNSGVFRRDDNI-RLTPO	255
MHCK A	692	WVVELIDRSPPSSNGQPIILCSIEPLLVGEFKKNNNSNYGAVLT-N--RSTPO	738

Figure 2A

human	eEF-2K	257T.	306
C.elegans	eEF-2K	240	AFSHFTFERSGHQMIVVDIQGVGDLYTDPQIHTVVGTDYGDGNLGTGRGMA	289
mouse	eEF-2K	256	AFSHFTFERSGHQLIVVDIQGVGDLYTDPQIHTTEKGTDFGDNLGVRGMA	305
MHCK A		739	AFSHFTYELSNQMIVVDIQGVDDLYTDPQIHTPDCKGFGGLGNLKGAGIN	788
human	eEF-2K	307E.....A.....R.....N.K.....	354
C.elegans	eEF-2K	290	LFFHSHRCNDICETMDLSNFEELSPPEIEATEVAMEVAAKQKSCIVPPPTV	339
mouse	eEF-2K	306	LFFYSHACNRICQSMGLTIPFDLSPREQDAVNQSTRLLQSAKT--ILRGTE	353
MHCK A		789	KFITTHKCNVCAILD	805
human	eEF-2K	355V...G....-RP.....	400
C.elegans	eEF-2K	340	FEARNRISSECVHVEHGISMDOQLRKRKTL---NQSSDLSAKSHNEDCV	386
mouse	eEF-2K	354	EKCGSPRIIRILSS---RPPLL-LRLSENSGDENMSDVTDFSLPSSPSA	399
human	eEF-2K	401-.....S.....AS.....HL....E.....G	449
C.elegans	eEF-2K	387	CPECIPVVEQLCEPCSEDEEEDDYPRSEKSGNSQKSRSRMSISSTRSS	436
mouse	eEF-2K	400	TEHSQKLDH-LHWPFVFGDLDNMGPRDHRMDNRDSENSGDSGYPSSEKRS	448
human	eEF-2K	450	-E.....-...YS...-KY.....K.....S....	494
C.elegans	eEF-2K	437	GDESASRPKCGFVDLNSLRQRHDSFRSSVCTYSMNSSRQTRDTEKDEFW	486
mouse	eEF-2K	449	-DLDDPEPREHG--HSGNR--RHEDEDSLGS-SGRVCVETWNLLNPSRL	493
human	eEF-2K	495A.....EK.....I.....	532
C.elegans	eEF-2K	487	KVLRKQSVPANILSLQLQQAANLENDEDVPQVTGHQFSVLGQIHIDLSR	536
mouse	eEF-2K	494	HLPRPSAVALLEVQRNLALDLGRKIGK-----SVLGKVLHLMVR	531

Figure 2B

601-1-098CIP

human	eEF-2K	533G.....Q.....V.....N.....	565
C.elegans	eEF-2K	537	YHELGRFVEVDSEHKEMLESENDA RVPKYDKQSAIFHLDIARKCGILE	586
mouse	eEF-2K	532	YHEGGRFCEKDEE-----WDRE SAIFHLEHAADLGELE	564
human	eEF-2K	566	596
C.elegans	eEF-2K	587	AVLTSAHIVLGLPHELLLKEVTVD DLFPNGFGEQENIGIRADKGGQKPCDLEE	636
mouse	eEF-2K	565	AIVGLGLMYSQLPHHLLADVSLKE -----TEENKTK-----	595
human	eEF-2K	597Q.....S.Q.....L.....	645
C.elegans	eEF-2K	637	FGSDLMETIAAEMGDKGAMLYMAHAYETG QHLPNRRRTDYKKSIDWYQRVV	686
mouse	eEF-2K	596	-GFDYLLKAAEAGDRHSMILLVARAFDTG LNLSPDRCDWSEALHWYN TAL	644
human	eEF-2K	646	-----M.....R.MM.....F...Y..E.D....	689
C.elegans	eEF-2K	687	GFQEEELDSDCCKTTFSSEAPLTRHEI LAKMAEMYKEGGYGLNQDFERA	736
mouse	eEF-2K	645	-----ETDCCDEG-GEYDGIQDEPQYAL LAREAEMLLTGGFGLDKNPQRS	688
human	eEF-2K	690Q.....	725
C.elegans	eEF-2K	737	YGLFNEAAEAAMEAMNGKLANKYYEKAEMC -----GE	768
mouse	eEF-2K	689	GDLYTQAEEAAEAAMEAMKGRLANQYYEKA EAWAQMEE	724

Figure 2C

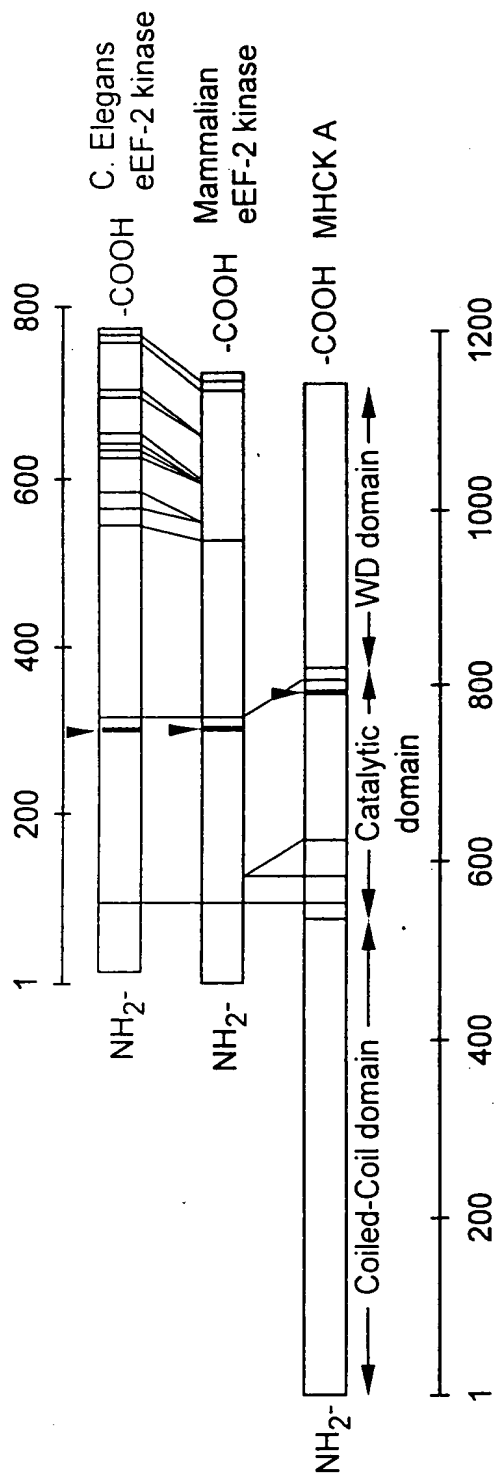


Figure 3

Current Biology

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 121 gtccttgctt ggtggcccgt gccaccgcct ccggagacgc tttccgatag gtggctgcag
 181 gccgcggagg tggaggagga gccgctgccc ttccggagtc cgccccgtga ggagaatgtc
 241 ccagaaatcc tggatagaga gcactttgac caagagggag tgtgtatata ttataccaag
 301 ctccaaagac cctcacagat gtcttccagg atgtcagatt tgtcagcaac ttgtcagatg
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Figure 5A

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Figure 5B

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09832292-121801

Figure 5C

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LFCCVCKRRKKDKTSDGPKLFLTEEDQKKLHDFEEQCVEMYFDEKDDKFNSGSEERIRVT
FERVEQMSIQIKEVGDRVNYIKRSLQSLDSQIGHLQDLSALTVDTLKTLTAQKASEASKV
HNEITRELSISKHLAQNLIDDVPVRPLWKKPSAVNTLSSSLPQGDRESNNPFLCNIFMKD

Figure 6A

EKDPQYNLFGQDLPVIPQRKEFNIPEAGSSCGALFPSAVSPPELRQRRHGVEMLKIFNKN
QKLGSSPNSSPHMSSPPTKFSVSTPSQPSCKSHLESTTKDQEPIFYKAAEGDNIEFGAFV
GHRDSMDLQRFKETS NKIRELLSNDTPENTLKHVGAAGYSECCKTSTSLHSVQAESCSRR
ASTEDSPEVDSKAALLPDWLRDRPSNREMPSEGGTLNGLASPFKPVLD TNYYYYSAVERN
LMRLSQSIPFVPVPPRGEPVTVYRLEESSPSILNNSMSSWSQLGLCAKIEFLSKEEMGGG
LRRAVKVLCTWSEHDILKSGHLYIIKSFLPEVINTWSSIIYKEDTVLHLCLEIQQQRAAQ
KLTFAFNQMKPKSIPYSPRFLEVFLLYCHSAGQWFAVEECMTGEFRKYNNNNNGDEI IPTN
TLEEIMLAFSHWTY EYTRGELLVLDLQGVGENLTDPSVIKAEKRS CDMVFGPANLGEDA
IKNFRAKHHCNSCCRKLKLPDLKRNDYTPDKIIFPQDESSDLNLQSGNSTKESEATNSVR
LML

Figure 6B

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MSQKSWIESTLTKRECVYIIPSSKDPHRCLPGCQICQQLVRCFCGRLVKQHACFTA
SLAMKYSDVKLGDFHNQAIEEWSVEKHTEQSPTDAYGVINFQGGSHSYRAKYVRL
SYDTKPEVILQLLLKEWQMELPKLVISVHGGMQKFELHPRIKQLLGKGLIKA AVT
TGAWILTGGVNTGVAKHVGDALKEHASRSSRKICTIGIAPWGVNIENRNDLVGRDVV
APYQTLNPLSKLNVLNHSHFILVDDGTVGKYGAEVRLRRELEKTINQQRIHAR
IGQGVPVVALIFEGGPNVILTVLEYLQESPPVPVVVCEGTGRAADLLAYIHKQTEEG
GNLPDAAEPDIISTIKKTFNFGQNEALHLFQTLMECMKRKELITVFHIGSDEHQDID
VAILTALLKGTNASAFDQLILTAWDRVDIAKNHVFVYGQQWLVGSLAQAMLDA
VMDRVAFVKLLIENGVSMMHKFLTIPRLEELYNTKQGPTNPMLFHLVRDVVKQGNLP
PGYKITLIDIGLVIEYLMGGTYRCTYTRKRFRLIYNSLGGNNRRSGRNTSSSTPQLR
KSHESFGNRADKKEKMRHNHFIKTAQPYRPKIDTVMEEGKKKRTKDEIVDIDDPE
TKRFPYPLNELLIWACL MKRQVMARFLWQHGEESMAKALVACKIYRSMAYEAKQ
SDLVDDTSEELKQYSNDFGQLAVELLEQSFRQDET MAMKLLTYELKNWSNSTCLK
LAVAAKHRDFIAHTCSQMLLTDMWMGRRLMRKNPGLKVILSILVPPAILLLEYKT
KAEMSHIPQSQDAHQM TMDSEN NFQNITEEIPMEVFKEVRILDSNEGKNEMEIQM
KSKKLPI TRKFYAFYHAPIVKFWFNTLAYLGFLMLYTFVVLVQMEQLPSVQEWIVI
AYIFTYAIEKVREIFMSEAGKVNQKIKVWFSDYFNISDTIAIISFFIGFLRFGAKWNF
ANAYDNHVFVAGRLIYCLNIIFWYVRLLD FLAVNQQAGPYVM MIGKMMVANMFYIV
VIMALVLLSFGVPRKAILYPHEAPSWTLAKDIVFHPYWMIFGEVYAYEIDVCANDS
VIPQICGPGTWLTPFLQAVYLFVQYIIMVNLLIAFFNNVYLQVKAISNIVWKYQRYH
FIMAYHEKPVLPPLIILSHIVSLFCCICKRRKKDKTSDGPKLFLTEEDQKKLHDFEE
QCVEMYFNEKDDKFHSGSEERIRVT FERVEQMCIQIKEVGDRVNYIKRSLQSLDSQI
GHLQDLSALTVDTLKTLTAQKASEASKVHNEITRELSISKHLAQNLIDDGPVRPSV
WKKHGVVNTLSSSLPQGDLESNNPFHCNILMKDDKDPQCNIFGQDLPVPQRKEF
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VSTPSQPSCKSHLETGTKDQETVCSKATEGDNTEFGAFVGHRDSMDLQRFKETS
KIKILSNNNTSENTLKRVS LAGFTDCHRTSIPVHSKQEKISRRPSTEDTHEVDSKAA
LIPVWLQDRPSNREMPSEEGTLNGLTSPFKPAMDTNYYYSAVERNLMRLS QSIPF
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FAFNQMKPKSIPYSPRFLEVFLLYCHSAGQWFAVEECMTGEF
RKYNNNNGDEIPTNTLEEIMLAFSHWTYEYTRGELLVLDLQGVGENLTDPSVIKA
EEKRSCDMVFGPANLGEDA IKNFRAKHHCNSCCRKLKLPDLKRNDYTPDKIIFPQD
EPSDLNLQPGNSTKESESTNSVRLML

Figure 7B

[illegible]

Figure 8A

FOBT2T" 2622E860

ESAEPLTQSDKKRETSHTTAAATGRSSHADARECAISTAQAEQAKLTQSTDSVSKEGNTNCKGEGMQVN
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KPCTCGPQEEKQDRDGNIPDNFREDLKYEQSISEANDETMSPGVFSRHLPKDARADFREPVAVSVASPEP
TDTALTLENVCDEPRDREAVCAMECFEASDQGTCTDIDSLVGTVPDNYSPQEICSVDTELAEQONKVS
LCSSNDKLTLEVFQQTQVSETSVSTCKSSKDGNSVMSPLFISTFTLNISHTASEGATGENLAKVEKSTYPLAS
TVHAGQEQSPSNSGGLDETQLLSENPNLVQFKEGGDKSPSPAADTTATPASYSIVSFPWEKPTTLTAN
NECFQATRETVTIADEVHPAKYLAVSIPEDKHAGGTEERFPRASHEKVSQFPSQVQVDHILSGATIKSTKEL
LCRAPSVPGVPHHVLLQPEGEGFCNSPLQVDNLSGDKSQTVDRADFRS YEENFERGSETKQGVQQSL
SQQGLSAPDFQQSLPTTSAAQEERNLVPTAPSPASSREGAGQRSWGTRVSVVAETAGEEDSQALSNVPS
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AASETGGKENVNNVSQDQEEKQLKMDHTAFFKKFLTCPKILESSVDPIDEISVIEYTRAGKPEPSETTPQGA
REGGQNDGNMGHEAEIQSAILQVPCQLGTILSENRSRQEGSMKQAEQIQPEEAKTAIWQVLQPSEGG
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PLEGFGEVPEIIFLIHRPENNIPIYATVEEELIGEFVKYSIRDGKEINFLRRESEAGQKCCCTFQHWVYQKTSG
CLLVTDMMQGVGMKLT DVGIA TLAKGYKGFKGNCMTFIDQFKALHQC NKYCKM LGLKSLQNNNQKQK
QPSIGKSKVQTN SMTVKKAGPETPGEKKT

Figure 8B



1 atgtcccaga aatctctggat taaaggagta ttgacaaga gagaatgtag cacaatcata
 61 cccagctcaa aaaatectca cagatgtact ccagtatgcc aagtctgcca gaatttaate
 121 aggtgttact gtggccgact gattggagac catgctggga tagattatc ctggaccatc
 181 tcagctgcca agggtaaaga aagtgaacaa tggctgttg aaaagcacac aacgaaaage
 241 ccaacagata cttttggcac gattaatttc caagatggag agcacaceca tcatgccaag
 301 tataattaga cttcttatga tacaaaaactg gatcatctgt tacatttaac gttgaaagag
 361 tggaaaaatgg aactgcccga gcttgtgac tcagtcctg ggggcatcca gaactttact
 421 atgcectcta aatttaaaga gattttcagc caaggtttgg ttaaagctgc agagacaaca
 481 ggagcgtgga taataactga aggcatacat acagtgtcca agcatgttgg ggatgccttg
 541 aaatcccat cctctcattc ctgagaaaa atctggacag ttggaatecc tcttgggggt
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 1501 gacattggat tagtagtaga atacctcatt ggtagagcat atgcagcaa ctacactaga
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 1621 tcaggaaata gaaatgagtc tgcagaaagt acgtgcact cccagttcat tagaactgca
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 2821 cggtcctgg actctttgc tgtgaatcaa catgcaggtc catatgtgac catgattgca
 2881 aaaatgacag caaacatgt ctatattgt atcatatgg ccagatgct gctgagcttt
 2941 ggagtggcac gcaagccat ctttgcga aaagagccac catcttgag tctagctga
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 3061 gttgttcaa gccagccatc ctgctctct ggtttttt ttaactcatt ctgcaagct
 3121 gtctacctc tctgcaata tatcatcat gtgaacctgt tgattgttt ctcaacaac
 3181 gttacttag atatggaac cattcaaat aacctgtgga aatacaaccg ctatcgtac

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Figure 9A



3241 atcatgacct accacagaaa gccctggctg cccccacctc tcactctgct gagecacgtg
 3301 ggccttctec tccgcgcct gtgtgtcat cgagctctc acgaccaaga agaggggtac
 3361 gttggattaa aactctacct cagtaaggag gatctgaaaa aacttcatga ttttgaggag
 3421 cagtgcgtgg aaaaatactt ccagtagaag atggaagatg tgaattgtag ttgtaggaa
 3481 cgaatccgag tgacatcaga aagggttaca gagatgtact tccagctgaa agaaatgaat
 3541 gaaaagggtg cttttataaa ggactcetta ctgtctttgg acagccaggt gggacacctg
 3601 caggatctct ctgccctgac tgtggatacc ctgaaagtc ttctgtctg tgacatttg
 3661 caagaggatg aggtctctct ggccaagaga aagcattcta ctgcaaaaa acttcccac
 3721 agctggagca atgtcatctg tgcagagggt ctaggcagca tggagatcgc tggagagaag
 3781 aaataccagt attatagcat gccctcttct ttgttgagga gccctggctgg aggcggcat
 3841 cccccaagag tgcagagggg ggcacttctt gagattacaa acagtaaaag agaggctaca
 3901 aatgtaagaa atgaccagga aaggcaagaa acacaaagta gtatagtgtt ttctgggggtg
 3961 tecttaaca ggcaagcaca ctcaaagtat ggccagtctt ttctggctcc ctctaacta
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 4081 gtgtggcaa ctgaacagga catccagact gaggttcttg ttcatctgac tgggcagacc
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 5521 atacctaca caccaaggtt cctggaagt ttcttaact actgccattc agccaaccag
 5581 tggttgacca ttgagaagta tatgacaggg gagtccgga agtatacaa caacaatgtt
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 6121 tacatcagcg tctcttggg acagccttc tgagctcac atctcttct gttcaaggc
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Figure 9A



6481 aaaagttatg tgatttcctc ctctgtcttt tccacaacat aggactttga atagcaatga
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 6601 taccaagtat actggtgaaa tctcgatggg ttccagatat tgcagtgaa tcatatgatg
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 7261 cctccaaag ttgtatatat aatattgcag gttaaattac tttatgctag gtctatgaa
 7321 gaaagatacg gtttcagact gaaaacatgt ttcacagggt tttgcttct tccagagcag
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Figure 9A

MSQKSWIKGVFDKRECSTHPSKPNHRCTPVCQVCQNLIRCYCGRLIGDHAGIDYS
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 EIICMIQNTFNFSLKQSKHLFQILMECMVHRDCITIFDADSEEQQDLDLAILTALLK
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 KLLIEYGVNLHRFLTIPRLEELYNTKQGPTNTLLHHLVQDVVKQHTLLSGYRITLIDI
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 KHEPIAHLLDGQDKAEQVLPTLSCTPEPMTMSSPLSQAQIMQTGGGYVNWAFSEG
 DETGVFSIKKKWQTCLPSTCDSRSSRSEQHQKQAQDSSLSDNSTRSAQSSECSEVGP
 WLQPNTSFWINPLRRYRPFARSHSFRFHKEEKLKICKIKNLSGSSEIGQGAWVKA
 KMLTKDRRLSKKKKNTQGLQVPIITVNACSQSDQLNPEPGENSISEEEYSKNWFTV
 SKFSHTGVEPYIHKMKTKTEIGQCAIQISDYLKQSQEDLSKNSLWNSRSTNLNRNSL
 LKSSIGVDKISASLKSPQEPHHHYSIAIERNLMLRLSQTIPFTPVQLFAGEEITVYRLE
 ESSPLNLDKSMSSWSQRGRAAMIQVLSREEMDGLRKAMRVVSTWSEDDILKPGQ
 VFIVKSFLPEVVRTWHKIFQESTVLHLCLREIQQQRAAQKLIYTFNQVKPQTIPYTP
 RFLEVFLIYCHSANQWLTIEKYMTGEFRKYNNNNGDEITPTNTLEELMLAFSHWTY
 EYTRGELLVLDLQGVGENLTDPSVIKPEVKQSRGMVFGPANLGEDAIRNFIKHHHC
 NSCCRKLKLPDLKRNDSYPERINSTFGLEIKIESAEPPARETGRNSPEDDMQL

09832292-121801

Figure 9B

GTATCAGGACTCAGCCCATTTCCCCCTCTGGTCTGAGAAATGGAGGCCGAAGAGTGATCTAGAAAGTGTAAATTGAGCCCTAAATCTATGTCTAGTTAC
TGGGGTCTTGGGGAGACAGGAGAGATCCACGGGTTCGGGCTCCAGGACTCAGGTCACTAATGGAGGTGGCTTGGCTTGTCTATGTGCTGT
GGCCACAGCCACTGGCAGGCAAGCGAGGTCAGTCACGGCTGTGCCAGGAAGAGGGCTGGTCTTTGGCTCCTGTCTCCCGGGTCTAGCCCC
AAGCTGGCCAGCGGTTGACTGGCTCCCTGGCCCGGCCAGCCTCTGTGACCCCTATATGCCACAGGACATGACAGGCCGCCGCGCGGCGCTA
GGTCCGGAGTCCAGAAAGGGCTGTCTCCATGACAGGACACCCGCTGCGCTTCTCCGAGGCTCCCGGGCTCTCCAGACGCGCGGCTG
CTCAGACACAGGGCCGCCAAGGAGCGGACTCGGAGCGGGCTTGGCGGGGCACATGGGCCCGGCGGCTATAAATAGGGCGCGCTCTCCAAGCGCGCTGC
CCGGTGGGCCAGGCCAGGGGAGGACAGCAGCAGGTGACAGGCCCGGCCACCGGCTATAAATAGGGCGCGCTCTCCAAGCGCGCTGC
GGCGGGCGGCCACCCCGGGCTGGCGGGCTGGGAGTGGGCTGGGGCGGGGGCGGACGGTGAGGACGCGGCCGCTGTGGATCCCCAGCCC
GTCCGGAGGGCCCCACCTCCGGGTGGCGGGCTGGAGGACAGGCGGACCGGCTATAAATAGGGCGCGCTCTCCAAGCGCGCTGC
AGCACCGGAGTACTGTCTAGCTGGCGGGCGGAGACCACTTATCAAGCAACGGTGTCTCACCCCAGCTCTGGAAGGACACCTTCTGTCTCCAT
CATTTGCTCAGTCAAGAGAGACCCAGCGCTATTGAGACCAACGCTCAAGTCCCGTCTGTCCGAGGACAGCGACGTCAAGTTCACTGCATCGT
CACAGGATACCCAGAGCCAGGGTGACCTGTACAAGATGATACGGAGTGCACCGCTACTGTGGCTTGGCCAAATATGAGATCACTCATCAGGCCA
ACGCCACACTGCAGTGTACAGGTGTGAGAAAGATGCGGCCATCTACCGGCTCTGCCAGAACAGCAAGGGCAATTGTCTCTGTCTCAGGG
GTCTGGAGGTGGCCACCATGACTGATCAAGATCCACACGGCTGTTCGCCAAGTTGAAGCGCAAGGCTGGGCAAGACTGCGCGAGATCGAGCA
GAGCTGGAAGCACGAGAAAGCGGTGCTTGGGAGGTGCACACTTCGCAAGCTCAGCCCCGACCGCTTCCAGCGAAAGCGGCGATTGAGCGGGCT
CAAGCCCGGGCCCTCGTCCCTACCAGGGAGCCTGAGGTGGGACCCCTGGCGCTTGGCAGGAGGAGACTGAGACTGAGACTGCTCAGCTCAGGCTT
TGGGCTGTAAACAGTTTGTCTCTGAGAAAGTGACCAACCGGAGGCTGCCCGGAGATGGAGAGGACGAGGAACTCCAAGCAAGCGCTGC
ATCTGTACGCCATGGAGCTGGGCTCAGAGAGCCCTCAAGAGGAGTGGGGCCAAAGAAAGAAAGATGAGGAATCCAAGCAAGCGCTGC
GGAAGCCAGATTAGAAAGGCACCCCAAGCCCGCTTCTCAGAAAATGCAATCCCCAGCTCAGAGAGCTGAGGAGGCTCTGTGGGACTCAGGGGCC
TGGGCACTCCAGACAAGGCCAGAGGCCCTGGCCAGGCCAGCCAGGAAGTGTATTTCTCTTGAAGGACATGTAACCTTGAAGGACATGTAACCTTGA
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GGGTGCTGGGCTCTGGCCAGCCCAACACTCTTGAACCCCAAGCCGACTAGCCCTTCAACAGAAAGAGATTTGGCCCTCCAAAGCCAAAGAG
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GGCGCATCTGGAGCGTGTGGAGAAACACCTGGTGCAAGTGCACAGCCCTGCTGAGCCCCGTGACCTCCCGCCCTCACCAGGCTCTCTG
GACCGTGAAGTGCAGGCTGGCCGCCAGGCCCTTGTGCTGTGCCAGAGGCTCTGGTCCAGCTCCCTCACTGTCCCTGCCATTTGTGTGTAG

Figure 10A

[illegible]

Figure 10A

MEVAWL VYVLGQQPLARQEGEQSRLVPGRGLVWLPLPRSSSWPAVDLAPARPRGPLICHTGHEQAGREP
PGSSTKGPVLHDQDTRCAFLPRPPGLQTRRYCRHQGRQSGLAGPGAGTWAPPGVSKPRCPGRARPGEQQQ
VTTARPPAINRGARQPRAGAAAAGRPGAGAWRTGEAAAAGAVGEGGAMGSRRAPTRGWAGGRSGAGGDGE
DDGPVWIPSPASRSLSVRPETSLSSNRLSHPSGRSTFCISIAQLTEETQPLFETTLKSRVSSESDVRFTCIVTGYPEP
EVTWYKDDTELDRYCGLPKYEITHQGNRHTLQLYRCREDAAIYQASQNSKIVSCSVLEVGTMTYKIHQRWF
AKLKRKAAAALREIEQSWKHEKAVPGEVDTLRLKLSPDFRQRRRLSGAQAPGPSVPTREPEGGLTAAWQEGETETA
QHSGGLINSFASGEVTTNGEAAPENGEDGEHLLTYICDAMELGPRALKEESGAKKKKDEESKQGLRKPELEKA
AQSRSENCEIPSSDEPDSCGTQGPVGEVQVQTPRGRAARGPGSSGTDSTRKPASAVGTPDKAQKAPGPGQEVYF
SLKDMYLENTQAVRPLGEEGPQTLVVRAPGESPKGAPLARSEGVPAGPQTHSLTPQTRPFNRKRFAAPPKPG
EATTDSPISLSQAPECCGAQSLGKAPPQASVQVTPPARRRHGTTRDSTLQGAHQRTPEVLECCQTTAPTMSASSS
DVASIGVSTSGSQGHEPMDMETQEDGRTSANQRTGSKNVQADGKIQVDGTRGDGTQTAQTRADRKTQVDAGT
QESKRQSDRSAQKGMMTQGRAETQLETTQAGEKIQEDRKAQADKGTQEDRRMQGEKGMQGEKGTQSEGSAPTA
MEGQSEQEVATSLGPPSRTPKLPPTAGPRAPLNEICFVQTPEGSCFPKPGCLPRSEEAVVTASRNHEQTVLGPLSGNL
MLPAQPPHEGSVEQVGGERCGRPQSSGPVEAKQEDSPFQCPKEERPQGGVPCMDQGGCPLAGLSQEVPTMPSLPGTG
LTASPKAGPCSTPTSQHGSTATFLPSEDQVLMSSAPTLHLGLGTPTQSHPPETMATSEGACAVPDVEGRTPGPRSC
DPGLIDSLKNYLLLLKLSSTETSGAGGESQVGAATGGLVPSATLTPTVEVAGLSPTSRRLERVENNHLVQSAQTL
LSPCTSRRLTGLLDREVQAGRQALAAARGSWGPGSSLTVPVAVVDEEDPGLASEGASEGEVLEGPGLLGASQES
SMAGRLGEAGGQAAPGQPSAESIAQEPSQEEKFPEALTGLPAAATPEELALGARRKRFLPKVRAAGDGEATTPEER
ESPTVSPRGPRKSLVPGSPGTPGRERRSPTQGRKASMLEVPRAEEELAAAGDLGSPKAGGLDTEVALDEGKQETLAKP
RKAKDLLKAPQVIRKIRVEQFPDASGSLKLWCQFFNILSDSVLTWAKDQRPVGEVGRSAGDEGPAALAIQASPVDC
GVYRCTIHNEHGSASTDFCLSPVLSGFISREEGEVGEIEIEMTPMVFAGKLADSGCWGDKLFGRLVSEELRGGGYGC
GLRKASQAKVIYGLEPIFESGRTCHIKVSSLLVFGPSSETSLVGRNYDVTIQGCKIQNMSREYCKIFAAEARAAPGFGEV
PEIPLYLIYRPANNIPYATLEEDLGKPLESYCSREWGCAEAPTASGSSEAMQKCCQTFQHWLYQWTNGSFLVTDLAGV
DWKMTDVQIATKLRGYQGLKESCFALLDRFASHQCNA YCELLGLTPLKGPEAAHPQAKAKGSKSPSAGRKGSQ
SPQPKKGLPSQGTRKSPSSKATPQASEPVTQLLGQPPTQEEGSKAQGMR

Figure 10B

ATGAATAATCAAAAAGTGGTAGCTGTGCTACTGCAAGAGTGCAAGCAAGTCTGGATCAGCTCTTGTGGAAAGCGCCAGATGTGTGCGAAGAGGACAA
GAGCGAGGACGAGCTTTACTCCCAAGGAGTTAAGGACCTGATCCAGGAGCAAGAAATGAAGTGGCCCTTCGTGCCTGAAAGAT
GGCAGTAAACAAAGCCGTGGGCCAGAGGACAAAACAACTGAAGGATGTGATTGGCGCGGTGCGAGCTTACTGGCTCCCTGAGGGCCTCC
ATCCTCGTCGGGACTGTGGCTGCGGGGCTATTGCTTCTTGGTGGACCGGTTCCTGTATGGCTCGACGTCTCTGGAAAACTTCTGCAGGTCGCC
AAAGGTCTCCACAAGTTGCAGCCAGCAATGGCCCAATTGCCCGCAGGTGTTATTCGCCAAGCCGAAATCTCCGTGAATCAGGAAAACTTTTAAAAAGCA
GAGTATATTCTGAGCATCTAATAAGCAACAATGAGCAACGGGTACCTGGCTGTACAGAAATGAAGTGAAGGTCTCTGGTGCAGTCTGGTCTGTATA
CAGATCAGAGGCGATCTTGCAAAAGCTGGGTATGTGTACGAAGCAGACAGATTAAATATGGGCTCCATTGTAGGATATTGGCACTTCTCCTCAGCCG
GATAAAAGGGCTCTCCAGCTGTAGGTATACTGGCAGACATCTTTTCTTCCATGAGCAAGAACGATTATGAAAAAGTTTAAAAACAATCCACAAGATTA
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TCACAGCTGTGAATATCCGTGGCAGCTGTTATTGTCTACAGTAGTTTCAATGACTGCTCCAGATTTGAAAAACCTTACAGATCTGTGTGTAAGCCAAAGA
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CCAGAACTCAGGACAGAGAAGCTCTGTCTCAAGAGTTATGTCTGTATTTCCCAAGTGGAAAGAACTTTCCAAAAATCCTTTGACACCTATTCCACAGCA
ACAGATCTTATGTTCCCGAGATTTCCGAGTTCGAGTGGATGGATAAACTTATCTTCATGGGCAAGGGGATTTCCAAAAATCCTTTGACACCTATTCCAAAA
CCATACTTCGGTGTGAAGTATTTGAAAGTGAATGTGGAAACAAACAAAAATGAAACAGAAAGATGCAAAACACAGGAGTCTGCATCACTGCTCTAAAAAC
AGAAATAAAACATCTGTGAGTACTACTCAAGAAAAGCCACATTTGTCAAGACACAGGAATATCTTCTCCCTTAATGGTAAAGATGTTCA
GAGGAACTCAGAAAGGGAGGAAGAGAACTGGACCCATTTCTGATGCAATTCGAGTCTCTTGGATCAAGATGTGGAGACTGAGACTGAGCCATCGG
ACTACAGCAATGGTGAAGGAGCTGTTTTCAAAGTCTGTAGTGGCAGCCAGACTTCCAGTCTTGGAGCAACTTATCAGGGTTAGTTCTCTGCAA
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CTTCTCAAAATCAGCCACAGCAACAGATGCCCTTGACACCCCTCTCGCCTCATATACCCAGGCAATTTCTTGGCCCTGGTGCAAGGCTCTAGAAAG
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GGTAGGCCCAAGAAATATGGGCAACATCTTTCAGTCCAAAGAAAGAAAGCCTTTGAAATAATTTGTGAGTTTCCAGAAACCAACTGCGATGTCAAAAGAC
AGGCAGGGAAAGACAGCGAGAAAGAAATAGTGAAGAGAGCGCAGGCCCTACATTTAAAGCTAGTCCCTCTGCTTCAACCCCTAAATCTGG
AGAAAGCTAGAAAGTCAACCTTTCAGAGGCTCTGCACAAATCTCTGGGAAACATTTCCATGCTGCCATGTAGTCTTCAACCCCTAAATCTGCT
CCTGTTCAAAATCTGACTCCAGAAAAGTGTGGCCAGTCGCAGAGCAGGGCATCGACCCCTGATGCTCCACAGTGGATGAGGAGGGGCAACTGCT
CGACAGCATGGATGTTCCCTGCAAAATGGGACGGCTCTCATAGCTGTGCATTTCTGAGACAGCCGCTGTGTGACAGGGGGGAGACCCCAACTTCCCTC
TGTAAGCGGTAAACATCTCTCCCTGCTCCTCAGCGGACTGCATACCAAGAGGAAAGGAAATCAGCCTGGAAACATGCTGAAATCTCAGTGGGAGTTTC
CAGCTCATCTCAGTGTGGTGAATCACTGCAATTTTCCAGTGGTTCTTGAGGGGGAAGCCCTTGGTCTCTATCTGAAATTCAGTGGGAGTTTC
TTGGGTTTCATTGGCCGGAAAGATGAGGAAAAGAGATCTTGAAGGCTCGCACTTGCAACCTGATGACTTTGAAAAGCTGTGGCAGGATGAGGCATGA
TTGGCTGTTTCAGAGACTAGAGAAATACGGGGTTTTTAAGCCCACTCACTCCACCGGACATAGTCTCTTTTGTAAATAATTCAAAAAAATCTGAA
CTGTGGACGGCCAGGAAACTATTGCTATTGGGGGACTACTTGACTGTGAAGAAAAGGACAGAAAGAAATGCTTTTGGGTTCATCATCTTTCAT
CAAGAGAAATTTCTGGGAGGTATGTGGGAAAGACTATAAGGAGCAGAAAGGGCTCTGGCAACACTTCACTGATGTGAGCGCAGATGACCGGCA
GCACTATGTGACAGAAATTAACAAGACTCTATGAACAAACATTTCCACCACAGATATTTCTACATCCCATCCCAATACTACTGATTTTAGAGGACAAG
ACAAATAAGGATGATCAGTGTGGAGCCTTACATACTGGGAGAAATTTGTAAATTTGTCAAAATTAACACGAAAGTGGTGAAACACAGAAATACAAAGCCCA
GAATATGGCTTGGCCTATGGCCATTTTCTTATGAGTTTCTAATCATAGAGATGTGTGTGGCGAATTTACAGGTGGGTACCCGGTAAATGGAAAAAGGAC
TCATCTACCTCAGATCCCCGATTCACCTCGTGTGACAGAAAGTTTTCACTACCAATTTTGGAAAGAGAGGAAATTTTTTACTTCTTTTAAATAACCCAGCAT
GTGGAAATGTAATGAAATCTGCCATCGTCTTTTGTGACTAGACCTTCAATGGAGAAACCA

Figure 11A

FOOTPRINT 2622E860

MNNQVVAVLLQECKQVLDQLLLEAPDVSEEDKSEDQRCRALLPSELRTLQAEAKEMKWPVFPVEK
WQYKQAVGPEDKTNLKDVGAGLQQLLASLRASILARDCAAAAVFLVDRFLYGLDVSGLLQVA
KGLHKLQAPATPIAPQVVIRQARISVNSGKLLKAEYILSSLISNNGATGTWLYRNESDKVLVQSVCIQI
RGQILQKLGMWYEAELIWAIVGYLALPQPDKKGLSTSLGILADIFVMSKNDYEKFKNPNQINLS
LLKEFDHLLSAAEACKLAAAFSAYTPLFVLTAVNIRGTCLLSYSSSNDPPELKNLHLCFAKEAFEI
GLLTRDDEPVTGKQELHSFVKAAGFLTTHRRRLHGETGTVHAASQLCKEAMGKLYNFSTSSRSQ
DREALSQEVMVIAQVKEHLQVQSFNSVDDRSYVPESFECRLDKLILHGQGFQKILDYTSQHHTSV
CEVFESDCGNNKNEQKDAKTGVCITALKTEIKNIDTVSTTQEKPHCQRDTGISSSLMGKNVQRELRR
GGRRNWTSDAFRVSLDQDVETETEPSPDYSNGEGAVFNKSLSGSQTSAAWSNLSGFSSASWEEVNY
HVDDRSARKEPGKEHLVDTQCSTALSEELENDREGRAMHSLHSQLHDLSLQEPNNDNLEPSQNQPQ
QQMPLTPFSPHNTPGIFLAPGAGLLEGAPGIEQVVRNMGPRNTSAHSRPSYRSASWSSDSGRPKNMG
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FHRVLHNSLGNISMLPCSSFTPNWPVQNPDSRKSGGPVAEQGIDPDASTVDEEGQLLDSMDVPCTNG
HGSHRLCILRQPPGQRAETPNSSVSGNILFPVLSEDCITTEEGNQPGNMLNCSONSSSSSVWWLKSP
AFSSGSSEGDSPWSYLNSSGSSWVSLPGKMRKEILEARTLOPDDFEKLLAGVRHDWLFQRLTENTGV
FKPSQLHRAHSALLKYSKKSELWTAQETIVYLG DYLTVKKGRQRNFAFWVHHLHQEEILGRYVG
KDYKEQKGLWHHFTDVERQMTAQHYVTEFNKRLYEQNIPTQIFYIPSTILLILEDKTIKGCISVEPYI
LGEFVKLSNNTKVVKTEYKATEYGLAYGHFSYEFSNHRDVVVDLQGWVTGNGKGLIYLTDPQIHSV
DQKVFTTNFGKRGIFFYFNNQHVECNCHRLSLTRPSMEKP

Figure 11B

A	HeEF-2_kinase>	1 ALDD--EMLEKKA--SOPFGR--	AMRECEPTKASNPLHAQKAGSN--	WAKRATIEPDR--	DVNFED
	MHCK_B>	1 CT--ATLWKEPVFAE--	AFKATITLIS--	KSGAGRWVSKIGKXTPR--	PSMFED
	Melanoma_kinase>	1 SOLGLCAMEPTLSKEMG--	GHFIAVQCTWS--	EHDLKSHILHISLPEVNTWSSIKREDIVLH7CLRE	
	Kidney_kinase>	1 WORGRAAMQNLREEMD--	GERAWVSTWS--	EDDLKPKQVETKSELPPWVTHXIEQESTVLH7CLRE	
	Muscle_kinase>	1 WGDK--PGRVASELRLGGYGC--	KKASQAKVYG--	LEPFESRTECLVSSLLFPSPSSETSLGRNYDTIQG	
	Heart_kinase>	1 EGGR--RGQA--BELHFS--	EGVHRAATSTVHG--	LMPFKPGHACVTVHNAIAYGTRNNDELIORNYKJAAQE	
	Lymphocyte_kinase>	1 DAQETIIVG DYLVTKK--	ROANA--VWHH--	QEEILGRVCG--KEQKGL--	WHHFTG
	consensus	1 wt v i m s e G	ankakr l	i g yvik y v	y ed l
					I
	HeEF-2_kinase>	62 VPTOMEARLWGEENRRHRPPKO--	VPTMOXCIFELKORP--	GKPLH--	HE--GEK--KYNSSG
	MHCK_B>	56 KQOMIA--ADK--NSFHPKK--	IEFLQSCVEFYDT--	SSDLICG--	ABP--BEQYKYNSSG
	Melanoma_kinase>	74 QOORAAQKLTFA--OMKESI--	PYSPTETELVYCH--	SAGCIFA--	IECMA--GEPRKYNSSG
	Kidney_kinase>	74 QOORAAQKLTFA--OMKESI--	PYSPTETELVYCH--	SAGCIFA--	IECMA--GEPRKYNSSG
	Muscle_kinase>	75 QOORAAQKLTFA--OMKESI--	PYSPTETELVYCH--	SAGCIFA--	IECMA--GEPRKYNSSG
	Heart_kinase>	73 CYQNTL--YAKI--AAEAQPLEGFG--	PEIP--	PPANNIPAT--	EEETGEFVKYSIRD--
	Lymphocyte_kinase>	58 VERDVTQCHVTE--KRLYEONIP--	QIFV--	IPSTIL--	FILEDKTKGCSIS--
	consensus	81 v l q akw	fn kp	dip ml iflv r	f l e y i gef kynnm g
					II
	HeEF-2_kinase>	130 LTPQAFSHE--ERGGH--	EVV--	QV--	QV--
	MHCK_B>	124 NTPOSF--SHV--	SHV--	SHV--	SHV--
	Melanoma_kinase>	145 EIMLAF--SHV--	SHV--	SHV--	SHV--
	Kidney_kinase>	145 EIMLAF--SHV--	SHV--	SHV--	SHV--
	Muscle_kinase>	154 QKCT--	QKCT--	QKCT--	QKCT--
	Heart_kinase>	150 QKCT--	QKCT--	QKCT--	QKCT--
	Lymphocyte_kinase>	132 EYGL--	EYGL--	EYGL--	EYGL--
	consensus	161 afshwtyeyt g llvvd lqg	vg	d lTdggi t d	g fg gnlq gm F H CN C
					III
	HeEF-2_kinase>	196 ESK--	APF		
	MHCK_B>	190 QY--	QY--		
	Melanoma_kinase>	216 RKL--	PPDR		
	Kidney_kinase>	216 RKL--	PPDR		
	Muscle_kinase>	221 EL--	EL--		
	Heart_kinase>	217 RKL--	KS		
	Lymphocyte_kinase>	206 RKL--	PPDR		
	consensus	241 r l l i			
					IV
	HeEF-2_kinase>	196 ESK--	APF		
	MHCK_B>	190 QY--	QY--		
	Melanoma_kinase>	216 RKL--	PPDR		
	Kidney_kinase>	216 RKL--	PPDR		
	Muscle_kinase>	221 EL--	EL--		
	Heart_kinase>	217 RKL--	KS		
	Lymphocyte_kinase>	206 RKL--	PPDR		
	consensus	241 r l l i			
					V
	HeEF-2_kinase>	196 ESK--	APF		
	MHCK_B>	190 QY--	QY--		
	Melanoma_kinase>	216 RKL--	PPDR		
	Kidney_kinase>	216 RKL--	PPDR		
	Muscle_kinase>	221 EL--	EL--		
	Heart_kinase>	217 RKL--	KS		
	Lymphocyte_kinase>	206 RKL--	PPDR		
	consensus	241 r l l i			
					VI
	HeEF-2_kinase>	196 ESK--	APF		
	MHCK_B>	190 QY--	QY--		
	Melanoma_kinase>	216 RKL--	PPDR		
	Kidney_kinase>	216 RKL--	PPDR		
	Muscle_kinase>	221 EL--	EL--		
	Heart_kinase>	217 RKL--	KS		
	Lymphocyte_kinase>	206 RKL--	PPDR		
	consensus	241 r l l i			
					VII
	HeEF-2_kinase>	196 ESK--	APF		
	MHCK_B>	190 QY--	QY--		
	Melanoma_kinase>	216 RKL--	PPDR		
	Kidney_kinase>	216 RKL--	PPDR		
	Muscle_kinase>	221 EL--	EL--		
	Heart_kinase>	217 RKL--	KS		
	Lymphocyte_kinase>	206 RKL--	PPDR		
	consensus	241 r l l i			
					VIII

Figure 12

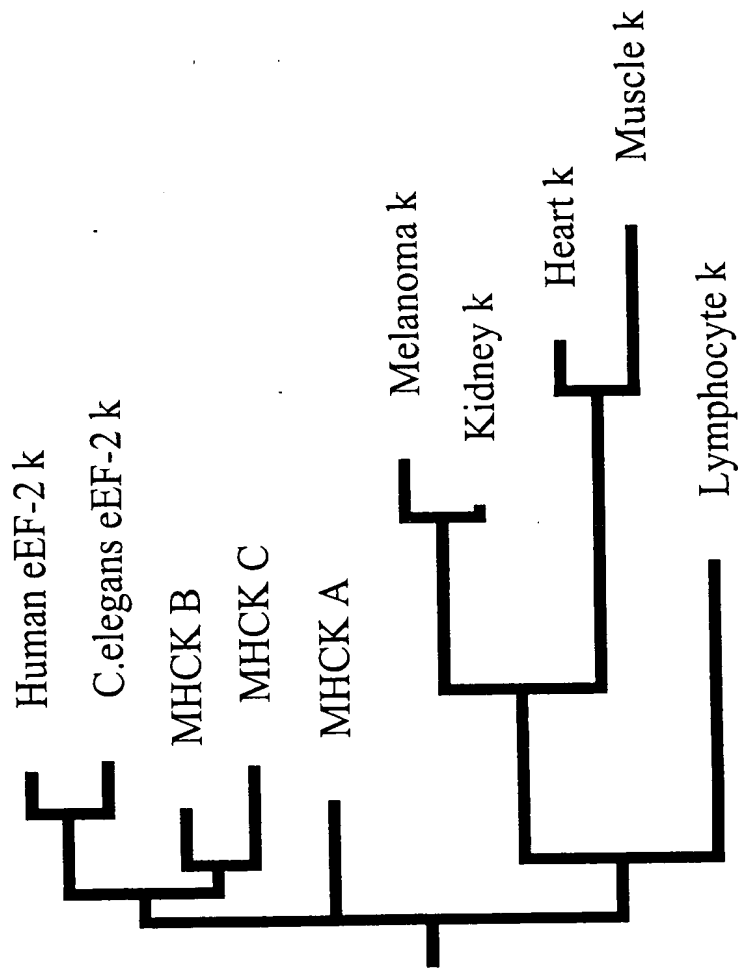


Fig. 1

Figure 13

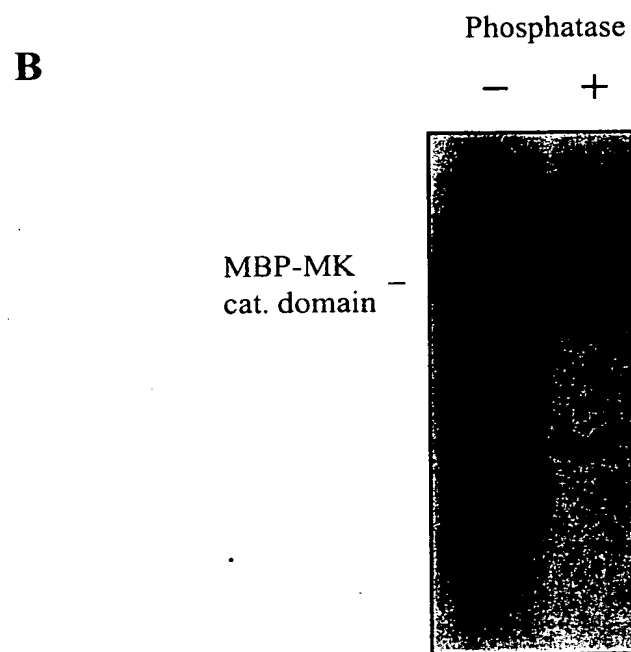
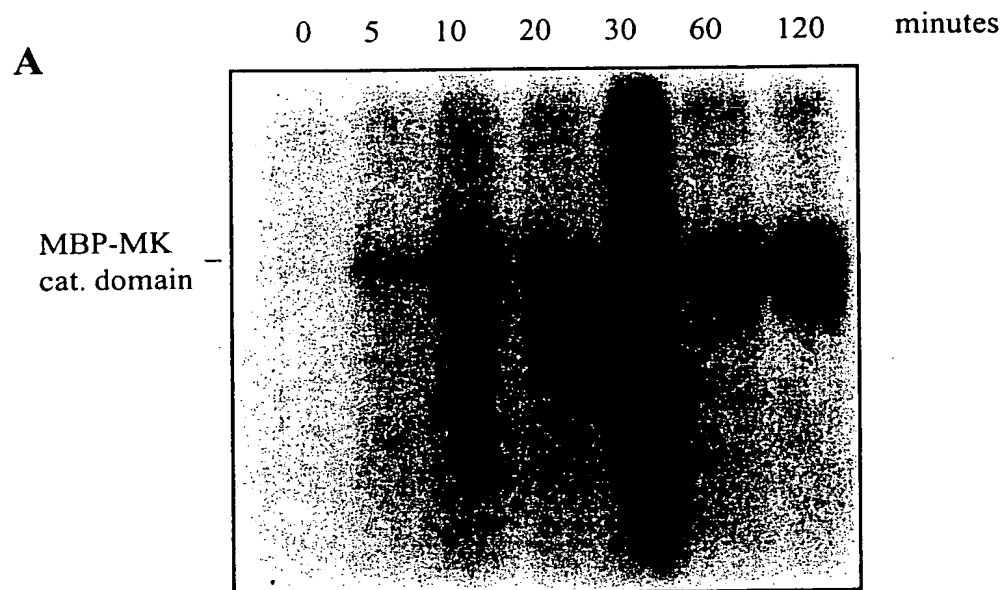
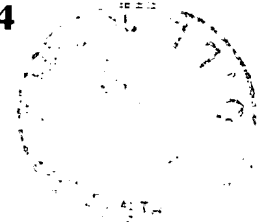


Figure 14

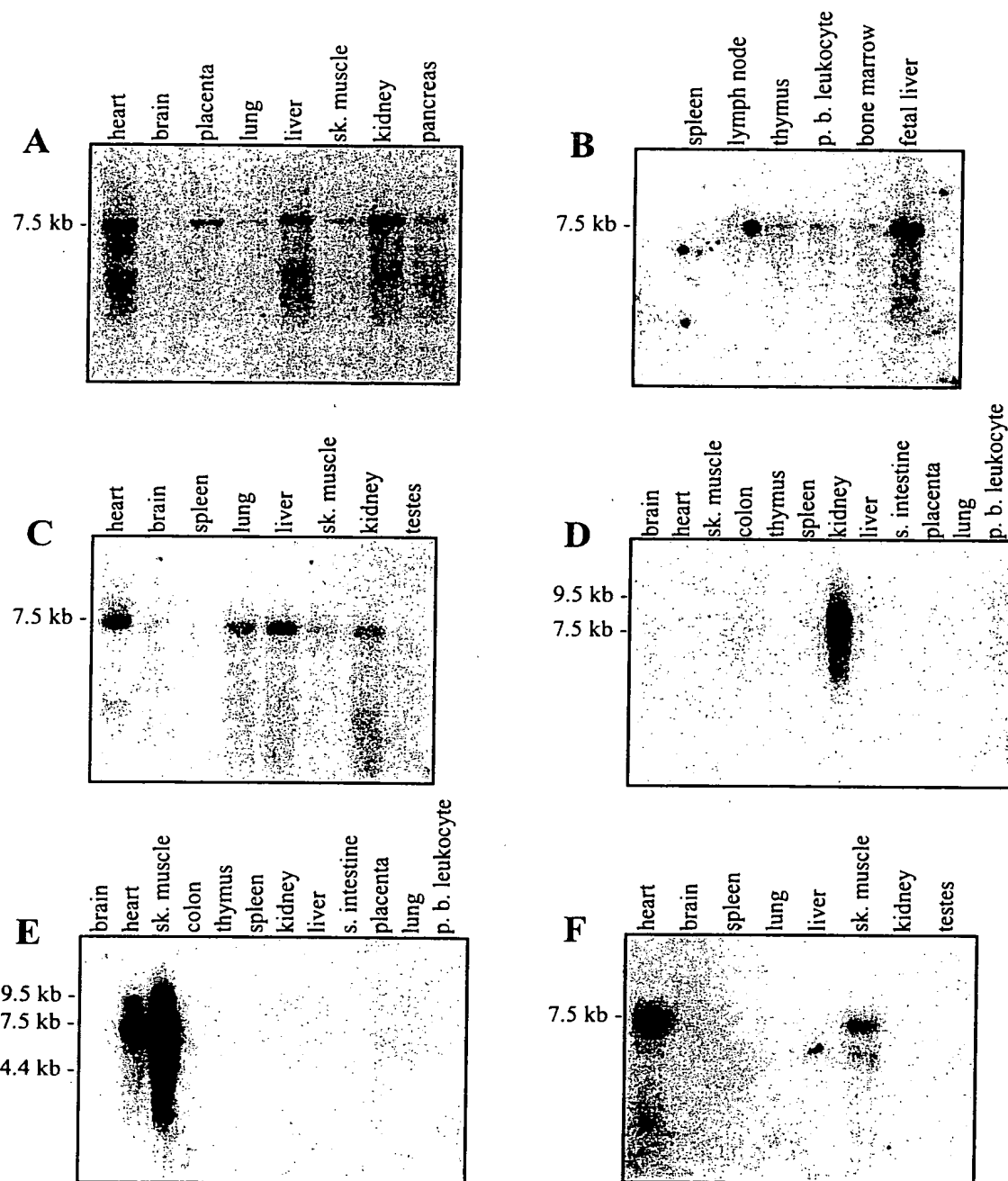


Figure 15

NK> 1 ASQNSWIESTLARECTYIPSSPHRCLPGCOICOOE XGRIKQICPTALAY
 KK> 1 ASQNSWIESTLARECTYIPSSPHRCLPGCOICOOE XGRIKQICPTALAY
 ME> 1

 NK> 51 KYSDVLCDFHNCATIEUSVEKHTCESTPLA MINCESEKAKI KUTREVA
 KK> 51 SAAKGE S LMSVEKHTCESTPLA MINCESEKAKI KUTREVA
 ME> 1

 NK> 121 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 121 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 15

 NK> 181 ANHVGDALHSS LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 181 ANHVGDALHSS LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 75

 NK> 241 ANHVGDALHSS LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 241 ANHVGDALHSS LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 135

 NK> 301 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 301 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 195

 NK> 351 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 351 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 255

 NK> 421 DIANM LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 421 DIANM LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 315

 NK> 438 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 438 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 375

 NK> 483 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 483 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 435

 NK> 543 NNRRSGRTSSST LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 543 NNRRSGRTSSST LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 494

 NK> 603 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 603 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 580

 NK> 663 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 663 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 583

 NK> 723 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 723 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 643

 NK> 783 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 783 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 703

 NK> 843 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 843 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 748

 NK> 903 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 903 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 808

 NK> 963 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 963 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 859

 NK> 1023 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 1023 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 919

 NK> 1070 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 1070 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 979

 NK> 1130 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 1130 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 1039

 NK> 1184 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 1184 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 1099

 NK> 1244 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 1244 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 1159

 NK> 1259 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 1259 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 1174

 NK> 1291 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 1291 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 1192

 NK> 1337 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 1337 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 1210

 NK> 1387 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 KK> 1387 LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC LKLEWOMELPKLVISVHCC
 ME> 1240

Figure 16

MELANOMA_KINASE> 1 -----MSQKSWIEST
KIDNEY_KINASE> 1 -----MSQKSWIKGV
MELASTATIN> 1 -----MYFETN
DmLTRPC1> 1 -----
CeLTRPC1> 1 MNLGYRRHYASSPEVWCTMESDELGVTRYLQSKGGDQVPPTSTTTGGAGGDNNAVPTTSSQAQQTNSGRQTTGMSSGDRLNEDVSATANSQAQLVPTPLFNQMRTES
CeLTRPC2> 1 -----MDRRKGSIVPAIKHKAVALSRANSVTVVEHESERETETQTKRR-----RKKQRTSSDKAPLNSAPRHVQKFDWKMDLHADISGKRGNSTTSHSGHATR
CeLTRPC3> 1 -----MKSSRRVKLRVHASLIENIRHTSSFLRLNAP-----RNSMCNANTVHSISSFRSDHLRSKSTKFDLNDNLFAILETEKLS-----
MTR1_LTRPC5> 1 -----MQDVQGPFGSGPGDAEDR
LTRPC6> 1 -----
trpc7_LTRPC2> 1 -----MEPSALRKAGSEQEGFGLPRRV

MELANOMA_KINASE> 11 LTKRECVYIIPSSKDPHRLPLPGCQICQQLVPCSGGLVVKCACTASLAMYKSDVKLG-----DHFNOAI
KIDNEY_KINASE> 11 FDKRECSYIIPSSKNPFRCTPVCQVCQNLICPCYCGRLIGAGIDYSWTSAAKGE-----SQGVSVHPTKSVPTFTNND
MELASTATIN> 1 -----MDSNPGCCGQFTNCIPPLPSAPSKNEES-----KQVETQPPKSVAPHTQSYPTSTVIE
DmLTRPC1> 7 WYFHPQPSWETNFQKREIKFIPCPKDDTYCGGQAQITQTIPGTESSPG-----LLPTCHRPQRTAYTIE
CeLTRPC1> 111 NMSLNRIHWRETTRECSRFIASSDLEHGGTRDAIRNIPELTSFELQKRSVALEQORSISNVNDINTQNMNYTKRGANKKTRIRHVSIAHAFQVE
CeLTRPC2> 97 AGSLKGGNMCECLKMGCSYFVPSQFSECGGERSKTEEVLEERSQNKHPLNHLTPGIEHVDTTADADNEVNLTPGR-----LQSHSEIVNVAIVYE
CeLTRPC3> 80 -----PPWENTFEKRTIRFAALPDQPECCGRLSAPSTPSTFS-----TLPVHLLKEQOTLIANNOTSTLAEFTVNG
MTR1_LTRPC5> 19 RELGLHR-----
LTRPC6> 1 -----
trpc7_LTRPC2> 25 TDLMGVSNLRRSNSSLFKSWRLQCPFGNNDQESLSSWIPENIKKKECVYFVSSSKLSDAGKVVQCQGYTHEQHLLEATKPHTFQGTQDPKLVQEMTAPDVT

MELANOMA_KINASE> 100 GSSYRKYVHSMUKIEVITCITLUREOMENPKLVSVHGGYCKEETUPLHPLCLOGLEAAVTTGAWITGAVNTGAAHVCDALKKHSR-----KCT
KIDNEY_KINASE> 93 GHTHSEKRYEEMTDLKDHILHMLKPKKPKLVSVHGGYCKEETUPLHPLCLOGLEAAVTTGAWITGAVNTGAAHVCDALKKHSR-----KCT
MELASTATIN> 64 GYSNKAAMHNSGDTKIDSLHMLKPKKPKLVSVHGGYCKEETUPLHPLCLOGLEAAVTTGAWITGAVNTGAAHVCDALKKHSR-----KCT
DmLTRPC1> 84 CAPPTACVFFRETRITRELICETFNHMLKLVGCGKANKLQAKLEIKKKLKAATTCGAWITGAVNTGAAHVCDALKKHSR-----KCT
CeLTRPC1> 221 CAPPTACVFFRETRITRELICETFNHMLKLVGCGKANKLQAKLEIKKKLKAATTCGAWITGAVNTGAAHVCDALKKHSR-----KCT
CeLTRPC2> 204 -----TANILHACVFFRETRITRELICETFNHMLKLVGCGKANKLQAKLEIKKKLKAATTCGAWITGAVNTGAAHVCDALKKHSR-----KCT
CeLTRPC3> 158 CAPPTACVFFRETRITRELICETFNHMLKLVGCGKANKLQAKLEIKKKLKAATTCGAWITGAVNTGAAHVCDALKKHSR-----KCT
MTR1_LTRPC5> 33 -----SGKRCREKVPFSGVANSVIFDMADHHPALNVAIVVEEOPAKSMIPVYKGVKASCTGAWITGAVNTGAAHVCDALKKHSR-----KCT
LTRPC6> 1 -----
trpc7_LTRPC2> 135 -----LSQYVKKVYVPPVQCTPSSVYHSHQHQHGLDVLNGLDTEPAKINIKRILNSLPSLVVQCTGAWITGAVNTGAAHVCDALKKHSR-----KCT

MELANOMA_KINASE> 207 MGVTEHNDV-----LVVAPQOLLNELSKINVLNLSHILVLDVPGVGYGALVALFELEHINRIHARIGQGVVAHIEGPNVILTDEQESFY
KIDNEY_KINASE> 199 MGVTEHNDV-----LVVAPQOLLNELSKINVLNLSHILVLDVPGVGYGALVALFELEHINRIHARIGQGVVAHIEGPNVILTDEQESFY
MELASTATIN> 171 MGVTEHNDV-----LVVAPQOLLNELSKINVLNLSHILVLDVPGVGYGALVALFELEHINRIHARIGQGVVAHIEGPNVILTDEQESFY
DmLTRPC1> 191 MGVTEHNDV-----LVVAPQOLLNELSKINVLNLSHILVLDVPGVGYGALVALFELEHINRIHARIGQGVVAHIEGPNVILTDEQESFY
CeLTRPC1> 328 MGVTEHNDV-----LVVAPQOLLNELSKINVLNLSHILVLDVPGVGYGALVALFELEHINRIHARIGQGVVAHIEGPNVILTDEQESFY
CeLTRPC2> 310 MGVTEHNDV-----LVVAPQOLLNELSKINVLNLSHILVLDVPGVGYGALVALFELEHINRIHARIGQGVVAHIEGPNVILTDEQESFY
CeLTRPC3> 267 MGVTEHNDV-----LVVAPQOLLNELSKINVLNLSHILVLDVPGVGYGALVALFELEHINRIHARIGQGVVAHIEGPNVILTDEQESFY
MTR1_LTRPC5> 142 LMRHLHRIEAAQEPFPHHPEDDGSGGQFCS-----SENTHUHLVETPPGGLDLEHILDEHIEFAGYGGTGSHEPVCLVNGDNPTRISRAVEQAAV
LTRPC6> 17 MGVTEHNDV-----LVVAPQOLLNELSKINVLNLSHILVLDVPGVGYGALVALFELEHINRIHARIGQGVVAHIEGPNVILTDEQESFY
trpc7_LTRPC2> 244 MGVTEHNDV-----LVVAPQOLLNELSKINVLNLSHILVLDVPGVGYGALVALFELEHINRIHARIGQGVVAHIEGPNVILTDEQESFY

MELANOMA_KINASE> 314 VCGSGGAAALILASVAVSONF-----LSMINTGNOVYRITGDPKTAQIKLOVPESTNSIMHIFES-----SREHIVHVSIMK-----PPG
KIDNEY_KINASE> 304 VCGSGGAAALILASVAVSONF-----LSMINTGNOVYRITGDPKTAQIKLOVPESTNSIMHIFES-----SREHIVHVSIMK-----PPG
MELASTATIN> 278 VCGSGGAAALILASVAVSONF-----LSMINTGNOVYRITGDPKTAQIKLOVPESTNSIMHIFES-----SREHIVHVSIMK-----PPG
DmLTRPC1> 298 VCGSGGAAALILASVAVSONF-----LSMINTGNOVYRITGDPKTAQIKLOVPESTNSIMHIFES-----SREHIVHVSIMK-----PPG
CeLTRPC1> 434 VCGSGGAAALILASVAVSONF-----LSMINTGNOVYRITGDPKTAQIKLOVPESTNSIMHIFES-----SREHIVHVSIMK-----PPG
CeLTRPC2> 414 VCGSGGAAALILASVAVSONF-----LSMINTGNOVYRITGDPKTAQIKLOVPESTNSIMHIFES-----SREHIVHVSIMK-----PPG
CeLTRPC3> 372 VCGSGGAAALILASVAVSONF-----LSMINTGNOVYRITGDPKTAQIKLOVPESTNSIMHIFES-----SREHIVHVSIMK-----PPG
MTR1_LTRPC5> 252 VCGSGGAAALILASVAVSONF-----LSMINTGNOVYRITGDPKTAQIKLOVPESTNSIMHIFES-----SREHIVHVSIMK-----PPG
LTRPC6> 126 VCGSGGAAALILASVAVSONF-----LSMINTGNOVYRITGDPKTAQIKLOVPESTNSIMHIFES-----SREHIVHVSIMK-----PPG
trpc7_LTRPC2> 352 VCGSGGAAALILASVAVSONF-----LSMINTGNOVYRITGDPKTAQIKLOVPESTNSIMHIFES-----SREHIVHVSIMK-----PPG

MELANOMA_KINASE> 415 LAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA
KIDNEY_KINASE> 405 LAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA
MELASTATIN> 379 LAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA
DmLTRPC1> 404 LAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA
CeLTRPC1> 535 LAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA
CeLTRPC2> 515 LAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA
CeLTRPC3> 471 LAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA
MTR1_LTRPC5> 356 LAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA
LTRPC6> 227 LAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA
trpc7_LTRPC2> 460 LAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA-----AAMHVDIARSDVAKHESPOA

MELANOMA_KINASE> 467 RFLTPLEELVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
KIDNEY_KINASE> 457 RFLTPLEELVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
MELASTATIN> 489 RFLTPLEELVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
DmLTRPC1> 456 RFLTPLEELVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
CeLTRPC1> 587 RFLTPLEELVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
CeLTRPC2> 567 RFLTPLEELVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
CeLTRPC3> 523 RFLTPLEELVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
MTR1_LTRPC5> 408 RFLTPLEELVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
LTRPC6> 279 RFLTPLEELVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
trpc7_LTRPC2> 512 RFLTPLEELVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S

MELANOMA_KINASE> 554 STPOLRKSHESFNRADKKEKMRNHFFITQPYRPKIDTVMEEG-----KKRKTDEIVDDDPETKREPTLNETLWACM-----V
KIDNEY_KINASE> 533 -----KYKHQRHSSNRNESAESTLHSGFTITQPYKPKKESIVLHK-----SRKKSKEQNVSDDPESTGELNELLVLAAM-----K
MELASTATIN> 564 -----PKRPAKLLMEDDEPPAKGKKK-----KKKEEEDDVPDPAVSRECEHEIMVAVIM-----K
DmLTRPC1> 534 -----ACKRSSTYQORYAGANSILVLTGLLPTSEMALFE-----FPENELLYSGFRNTHPSCCTSRLLFEK-----V
CeLTRPC1> 694 GVGGSVAVGNSFGNODPFLDPHNLSSGSRALSNHILWRSAGNFPANPMRPNLGDSDCGSEFDELSLTSASDGSQTEPDRFTS-----V
CeLTRPC2> 647 SNGGRNDVIGPSDAGRERMSSMQISINNRNSIISLFGNGGRK-----RESDDDDFNTEEANDMTPTPYSDHMAVNT-----K
CeLTRPC3> 601 -----SYFHRKRKIVQKELEF-----KKSDQNDNEEEDFSALHNSNELLWANTSHG-----K
MTR1_LTRPC5> 488 -----DRRR-----AEGKPAKEP-----TCQKWLDDLNQKSNHRLLELWANTSHG-----K
LTRPC6> 351 -----WDPHPGQGGESMYITSD-----KATSPSLDAGLGQAALHLLLNAP-----SLYKRSSGHVTFMTDTRDLWELVONRE
trpc7_LTRPC2> 583 -----NDRLRLLLPVPHVKINVCVSLR-----S

MELANOMA_KINASE> 638 RFLTPLEELVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
KIDNEY_KINASE> 613 RFLTPLEELVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
MELASTATIN> 628 RFLTPLEELVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
DmLTRPC1> 609 RFLTPLEELVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
CeLTRPC1> 804 RFLTPLEELVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
CeLTRPC2> 733 RFLTPLEELVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
CeLTRPC3> 653 RFLTPLEELVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
MTR1_LTRPC5> 534 RFLTPLEELVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
LTRPC6> 401 RFLTPLEELVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
trpc7_LTRPC2> 638 RFLTPLEELVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S

MELANOMA_KINASE> 743 MRLKSHKSWYVILSTVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
KIDNEY_KINASE> 723 MRLKSHKSWYVILSTVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
MELASTATIN> 738 MRLKSHKSWYVILSTVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
DmLTRPC1> 719 MRLKSHKSWYVILSTVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
CeLTRPC1> 914 MRLKSHKSWYVILSTVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
CeLTRPC2> 843 MRLKSHKSWYVILSTVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
CeLTRPC3> 763 MRLKSHKSWYVILSTVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
MTR1_LTRPC5> 638 MRLKSHKSWYVILSTVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
LTRPC6> 507 MRLKSHKSWYVILSTVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S
trpc7_LTRPC2> 744 MRLKSHKSWYVILSTVILKQFPMFPHVRYVQKQNPFGKQKIDIGLVYVILGRTCTYTPKREFLEH-----SLGNNRRSGRNTS-----S

Figure 17A

MELANOMA_KINASE> 1727 RRYNNKNGDENLPNTLLEELHLAFSEWTFYEYTRGELLVLDLGGVGENLTPDPSVIRABERSCDRVFQPAHLGEDAIFHBRKHHHCNSCCPAKILPLRPNHYTIKIFP
KIDNEY_KINASE> 1873 RRYNNKNGDENLPNTLLEELHLAFSEWTFYEYTRGELLVLDLGGVGENLTPDPSVIRABERSCDRVFQPAHLGEDAIFHBRKHHHCNSCCPAKILPLRPNHYTIKIFP
MELANOMA_KINASE> 1837 QDEPSDNLQPGNSTSESESTNSVRLIL-
KIDNEY_KINASE> 1983 FGLEIKTESAEPPAFIDGRNSPEDDQQL

Figure 17B

601-1-098CIP

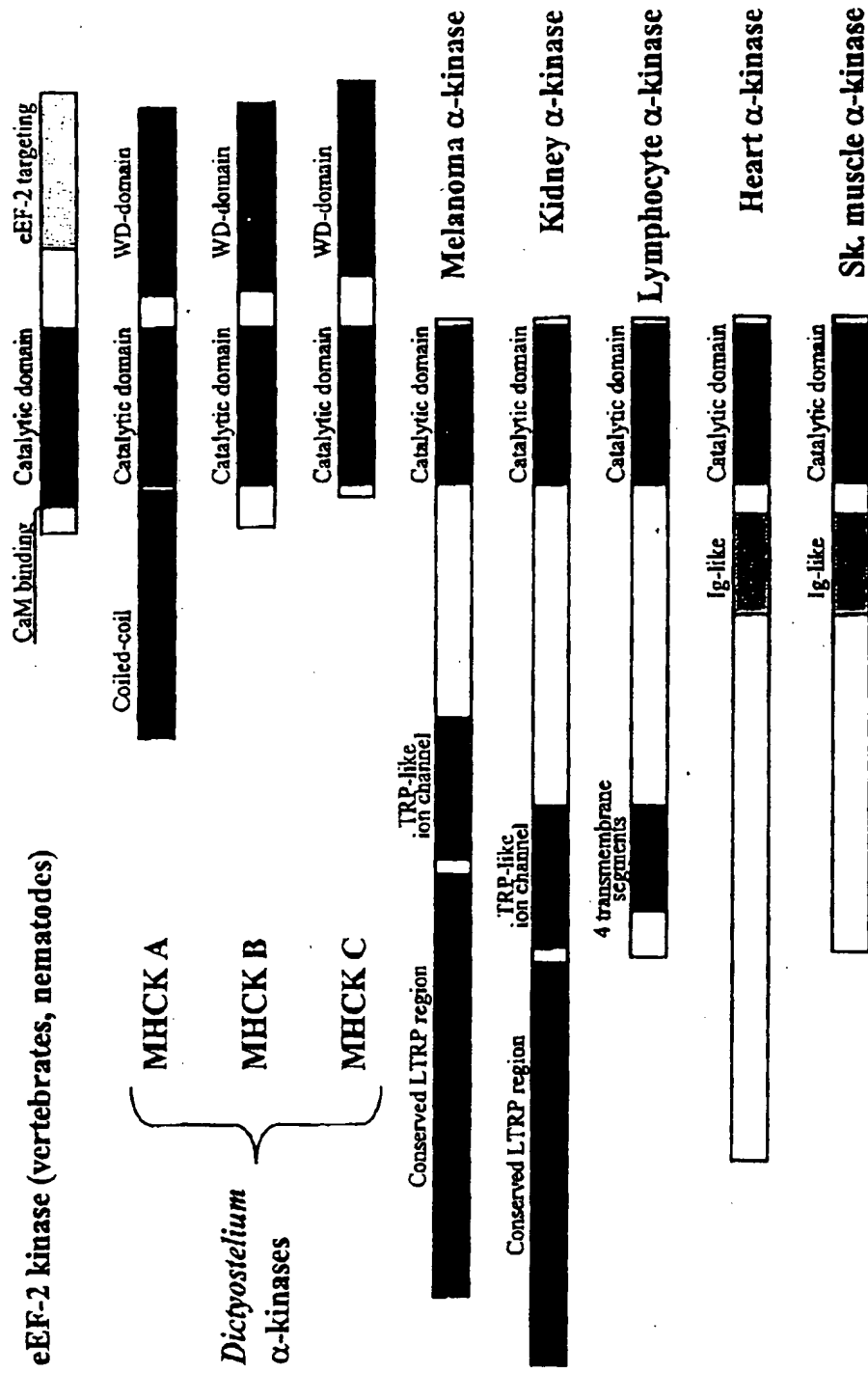


Figure 18

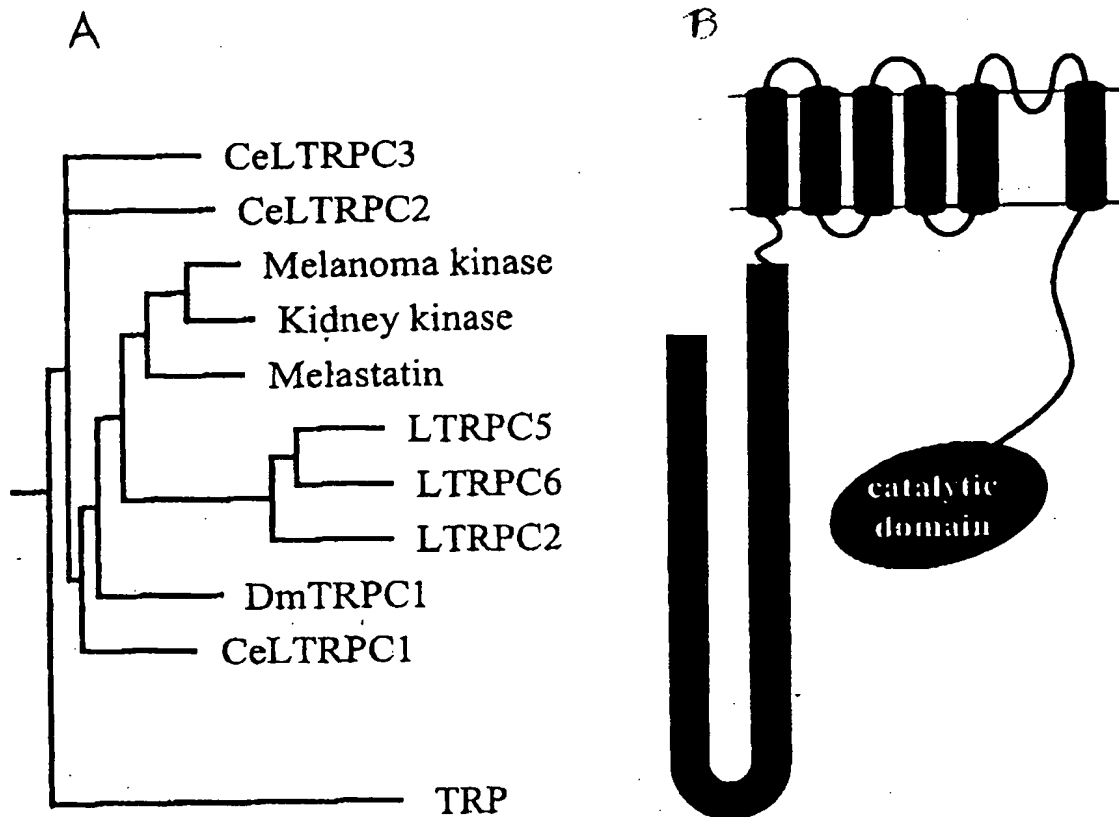
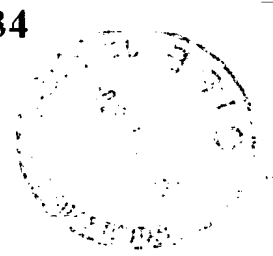


Figure 19